REMARKS

Status of the Claims

Claims 1-26 are cancelled without prejudice to or disclaimer of the subject matter recited therein. Claims 27-38 are pending. No claims are amended in this paper.

Office Action Summary

In the Office Action Summary, the box (9) indicating that the specification is objected to by the Examiner is checked. However, no explanation of the objection is present in the body of the Office Action. Applicants request clarification.

Claim Rejections under 35 U.S.C. § 102(b)

The Office Action of April 20, 2005 maintains the rejection of claims 27-38 under 35 U.S.C. § 102(b) as being anticipated by WO 97/48793. The Examiner states that the USPTO lacks the search capabilities that use Ktuple, Window and Diagonals, and that therefore the "Patent Office is unable to determine the percent similarity of the prior art sequence to the claimed sequence based on the claimed method of alignment and claimed parameters" (Office Action, page 2). The Examiner states that "Applicants could overcome the rejection by providing the necessary alignment using the claimed parameters" (Office Action, page 3).

To assist the Examiner, Applicants attach Appendix A, which shows a comparison of the amino acid sequences of sterol delta-14 reductase from soy clone SID ssm.pk0031.d12:fis (SEQ ID NO:8), src3c.pk009.c1:fis (SEQ ID NO: 6) and *Arabidopsis thaliana* (WO 97/48793). Amino acids conserved among all sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the

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sequences. The method parameters used to produce the multiple alignment of the sequences below was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS.* 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10 and default parameters for pairwise alignments are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5). Applicants believe that the sequence disclosed in WO 97/48793 does not fall within the scope of the pending claims since SEQ ID NOs: 6 and 8 share only 80.4 and 78% sequence identity with the sequence of WO 97/48793.

CONCLUSION

Based on the foregoing remarks, Applicants respectfully request reconsideration and withdrawal of the rejection of claims and allowance of this application.
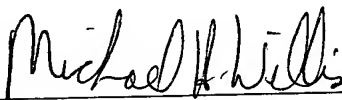
AUTHORIZATION

The Commissioner is hereby authorized to charge any additional fees which may be required for consideration of this Amendment to Deposit Account No. 13-4500, Order No. 2119-4293. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

In the event that an extension of time is required, or which may be required in addition to that requested in a petition for an extension of time, the Commissioner is requested to grant a petition for that extension of time which is required to make this response timely and is hereby authorized to charge any fee for such an extension of time or credit any overpayment for an extension of time to Deposit Account No. 13-4500, Order No. 2119-4293. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

Respectfully submitted,
MORGAN & FINNEGAN, L.L.P.

Dated: June 24, 2005   By: _____

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Appendix A

Appendix A shows a comparison of the amino acid sequences of sterol delta-14 reductase from soy clone SID ssm.pk0031.d12:fis (SEQ ID NO:8), src3c.pk009.c1:fis (SEQ ID NO: 6) and *Arabidopsis thaliana* (WO9748793). Amino acids conserved among all sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences. The method parameters used to produce the multiple alignment of the sequences below was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS. 5*:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). SEQ ID NO's: 6 and 8 share 80.4 and 78% sequence identity, respectively, with the sequence claimed in WO 9748793.

```
                *      *** **   *     **   **   * ****** *****    **  *  **   *  *  **
SEQ ID NO:8   MMESHVDLGFLLQALTPSWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCN
SEQ ID NO:6   MMESHVDLGFLLQALTPSWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCN
WO9748793     MLL-DMDLGVLLPSL----QSVYVLVFYFVYLAVAGEILPGKVIRGVLLSDGSQLRYRCN

                *** * **** *** **  * ***      ******* **  *  ****  *    *   *   ***
SEQ ID NO:8   GLLSLLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGS
SEQ ID NO:6   GLLSLLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGS
WO9748793     GLLALILLVAILGICAKLGIVSPLVVADRGLELLSATFIFCVLVTLALYVTGRSSSNKGS

                ***** ****  **************  **  *      *************  **  ***  ***
SEQ ID NO:8   SLKPHLSGNLIHDWWFGIQLNPQFMGIDLK-----AGMMGWLLINLSILMKSIQDGTLSQ
SEQ ID NO:6   SLKPHLSGNLIHDWWFGIQLNPQFMGIDLKFFFVRAGMMGWLLINLSILMKSIQDGTLSQ
WO9748793     SLKPHVSGNLVHDWWFGIQLNPQFMSIDLKFFFVRAGMMGWLLINLSILAKSVQDGSLSQ

                ****** *************************************** ****  ********* *
SEQ ID NO:8   SMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLMN
SEQ ID NO:6   SMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLMN
WO9748793     SMILYQIFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLLWIPFTFSIQGWWLLHN

                ****    ***  **  ***************** ******  ****** *  *****  *****
SEQ ID NO:8   SVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPPKVIGGKLLASGYWG
SEQ ID NO:6   SVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPPKVIGGKLLASGYWG
WO9748793     KVELTVPAIVVNCLVFLIGYMVFRGANKQKHIFKKNPKTPIWGKPPVVVGGKLLVSGYWG

                ********************  ****  ****************** **  ***********
SEQ ID NO:8   IARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTDEARCAEKYREIWAE
SEQ ID NO:6   IARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERRDEARCAEKYREIWAE
WO9748793     IARHCNYLGDLMLALSFSLPCGISSPVPYFYPIYLLILLIWRERRDEVRCAEKYKEIWAE

                *   **********
SEQ ID NO:8   YRKLVPWRILPYVY
SEQ ID NO:6   YRKLVPWRILPYVY
WO9748793     YLRLVPWRILPYVY
```

sequences. The method parameters used to produce the multiple alignment of the sequences below was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS.* 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10 and default parameters for pairwise alignments are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5). Applicants believe that the sequence disclosed in WO 97/48793 does not fall within the scope of the pending claims since SEQ ID NOs: 6 and 8 share only 80.4 and 78% sequence identity with the sequence of WO 97/48793.

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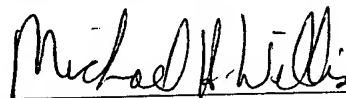
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